

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/521,230
Source: PT/10
Date Processed by STIC: 1/25/05

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PCT

RAW SEQUENCE LISTING

DATE: 01/25/2005

PATENT APPLICATION: US/10/521,230

TIME: 09:23:05

Input Set : A:\X15815.ST25.National.txt

Output Set: N:\CRF4\01252005\J521230.raw

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3 <110> APPLICANT: Songqing Na
4      Douglas Raymond Perkins
6 <120> TITLE OF INVENTION: Novel Proteins and Their Uses
8 <130> FILE REFERENCE: X-15815
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,230
C--> 11 <141> CURRENT FILING DATE: 2005-01-13
13 <160> NUMBER OF SEQ ID NOS: 24
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1479
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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24 <221> NAME/KEY: misc_feature
25 <222> LOCATION: (1)..(1479)
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35 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca gcatccgctt      240
37 gttgaaggcc accaagattt gtgtgacggg caaaagcaac ttccagtcct acagctgtgt      300
39 gaggtgcaat tacacagagg ccttccagac tcagaccaga ccctctggtg gtaaattggac      360
41 attttcctat atcggtctcc ctgtagagct gaacacagtc tatttcattg gggcccataa      420
43 tattcctaata gcaaataatga atgaagatgg cccttccatg tctgtgaatt tcacctcacc      480
45 aggaagcctg tgggatccga acatcactgc ttgtaagaag aatgaggaga cagtagaagt      540
47 gaacttcaca accactcccc tgggaaacag atacatggct cttatccaac acagcactat      600
49 catcggtgtt tctcaggtgt ttgagccaca ccagaagaaa caaacgcgag cttcagtggt      660
51 gattccagtg actggggata gtgaagggtg tacggtgcag ctgactccat attttcctac      720
53 ttgtggcagc gactgcatcc gacataaagg aacagttgtg ctctgcccac aaacaggcgt      780
55 ccctttccct ctggataaca acaaaagcaa gccgggaggg tggctgcctc tcctcctgct      840
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63 aaaccattgc agaagtgagg tcatccttga aaagtggcag aaaaagaaaa tagcagagat     1080
65 ggggtccagtg cagtggcttg ccactcaaaa gaaggcagca gacaaagtcg tcttccttct     1140
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71 ccagattcat ctgcacaaat acgtgggtgg ctactttaga gagattgata caaaagacga     1320
73 ttacaatgct ctcagtgtct gcccacagta ccacctcatg aaggatgcca ctgctttctg     1380
75 tgcagaactt ctccatgtca agcagcaggt gtcagcagga aaaagatcac aagcctgccca     1440
77 cgatggctgc tgctccttgt agcccaccca tgagaagca      1479
80 <210> SEQ ID NO: 2

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89 <223> OTHER INFORMATION: LP391
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98 20 25 30
101 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
102 35 40 45
105 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
106 50 55 60
109 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
110 65 70 75 80
113 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
114 85 90 95
117 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
118 100 105 110
121 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
122 115 120 125
125 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
126 130 135 140
129 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
130 145 150 155 160
133 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
134 165 170 175
137 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
138 180 185 190
141 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
142 195 200 205
145 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
146 210 215 220
149 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
150 225 230 235 240
153 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
154 245 250 255
157 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
158 260 265 270
161 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
162 275 280 285
165 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
166 290 295 300
169 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
170 305 310 315 320
173 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr

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Input Set : A:\X15815.ST25.National.txt

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181 Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
182          355          360          365
185 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
186          370          375          380
189 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
190 385          390          395          400
193 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
194          405          410          415
197 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
198          420          425          430
201 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
202          435          440          445
205 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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210 465          470          475          480
213 Asp Gly Cys Cys Ser Leu
214          485
217 <210> SEQ ID NO: 3
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220 <213> ORGANISM: Homo sapiens
223 <220> FEATURE:
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225 <222> LOCATION: (1)..(1614)
226 <223> OTHER INFORMATION: LP392
228 <400> SEQUENCE: 3
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233 aatcccgagg gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
235 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca gcatccgctt 240
237 gttgaaggcc accaagattt gtgtgacggg caaaagcaac ttccagtcct acagctgtgt 300
239 gaggtgcaat tacacagagg ccttccagac tcagaccaga ccctctggtg gtaaatggac 360
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243 tattcctaata gcaaatatga atgaagatgg cccttccatg tctgtgaatt tcacctcacc 480
245 aggctgcta gaccacataa tgaaatataa aaaaagtggt gtcaaggccg gaagcctgtg 540
247 ggatccgaac atcactgctt gtaagaagaa tgaggagaca gtagaagtga acttcacaac 600
249 cactcccctg ggaacacagat acatggctct tatccaacac agcactatca tcgggttttc 660
251 tcaggtgttt gagccacacc agaagaaaca aacgcgagct tcagtgggtg ttccagtgc 720
253 tggggatagt gaaggtgcta cgggtgcagg acttgcatgt cctaaagcac tggctgaagg 780
255 aagccaagag gatcactgct gctccttttt tctagaggaa atgtttgtct acgtgctgc 840
257 tccatatttt cctacttgtg gcagcgactg catccgacat aaaggaacag ttgtgctctg 900
259 cccacaaaca ggcgtccctt tccctctgga taacaacaaa agcaagccgg gaggtggct 960
261 gcctctctc ctgctgtctc tgcgtggtgc cacatgggtg ctggtggcag ggatctatct 1020
263 aatgtggagg cacgaaagga tcaagaagac ttctttttct accaccacac tactgcccc 1080
265 cattaaggtt cttgtggttt acccatctga aatatgtttc catcacacaa tttgttactt 1140

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267 cactgaattt cttcaaaacc attgcagaag tgagggtcatc cttgaaaagt ggcagaaaaa 1200
269 gaaaatagca gagatgggtc cagtgcagtg gcttgccact caaaagaagg cagcagacaa 1260
271 agtcgtcttc cttctttcca atgacgtcaa cagtgtgtgc gatggtacct gtggcaagag 1320
273 cgagggcagt cccagtgaga actctcaaga cctcttcccc cttgccttta accttttctg 1380
275 cagtgatcta agaagccaga ttcattctgca caaatacgtg gtggtctact ttagagagat 1440
277 tgatacaaaa gacgattaca atgctctcag tgtctgcccc aagtaccacc tcatgaagga 1500
279 tgccactgct ttctgtgcag aacttctcca tgtcaagcag cagggtgtcag caggaaaaag 1560
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292 <222> LOCATION: (1)..(531)
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302 20 25 30
305 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
306 35 40 45
309 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
310 50 55 60
313 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
314 65 70 75 80
317 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
318 85 90 95
321 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
322 100 105 110
325 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
326 115 120 125
329 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
330 130 135 140
333 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
334 145 150 155 160
337 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
338 165 170 175
341 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
342 180 185 190
345 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
346 195 200 205
349 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
350 210 215 220
353 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
354 225 230 235 240
357 Gly Asp Ser Glu Gly Ala Thr Val Gln Gly Leu Ala Cys Pro Lys Ala
358 245 250 255

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362      260      265      270
365 Glu Met Phe Val Tyr Val Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
366      275      280      285
369 Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
370      290      295      300
373 Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
374 305      310      315      320
377 Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala
378      325      330      335
381 Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe
382      340      345      350
385 Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro
386      355      360      365
389 Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu
390      370      375      380
393 Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys
394 385      390      395      400
397 Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
398      405      410      415
401 Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
402      420      425      430
405 Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
406      435      440      445
409 Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
410      450      455      460
413 Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
414 465      470      475      480
417 Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
418      485      490      495
421 Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
422      500      505      510
425 Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
426      515      520      525
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435 <212> TYPE: DNA
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449 aatccccgga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg      180
451 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcc a gcatccgctt      240

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VERIFICATION SUMMARY

DATE: 01/25/2005

PATENT APPLICATION: US/10/521,230

TIME: 09:23:06

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date